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SEQUENCE LISTING

<110> ONCOTHERAPY SCIENCE, INC.

THE UNIVERSITY OF TOKYO

<120> METHOD FOR DIAGNOSING HEPATOCELLULAR CARCINOMAS

<130> ONC-A0305P

<150> US 60/505,632

<151> 2003-09-24

<160> 28

<170> PatentIn version 3.1

<210> 1

<211> 1528

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (133).. (1308)

<223>

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ctcgccctac tgagcgagcg gcccggggcg ccgaggggtc cgcgccgcgc ggggcgcacc 120

gccctggccg cc atg tgc tcc cag ctc tgg ttc ctg acg gac cgg cgc atc 171

Met Cys Ser Gln Leu Trp Phe Leu Thr Asp Arg Arg Ile

1 5 10

cgc gag gac tac ccg cag gtg cag atc ctg cgc gcc ctc cgg cag cgc 219

Arg Glu Asp Tyr Pro Gln Val Gln Ile Leu Arg Ala Leu Arg Gln Arg

15 20 25

tgc tcc gag cag gac gtg cgc ttc cgg gcg gtg ctt atg gac cag atc 267

Cys Ser Glu Gln Asp Val Arg Phe Arg Ala Val Leu Met Asp Gln Ile

30 35 40 45

gcc gtc acc atc gtc ggc ggc cac ctc ggc ctc cag cta aac cag aag 315

Ala Val Thr Ile Val Gly Gly His Leu Gly Leu Gln Leu Asn Gln Lys

50 55 60

gcc ctc acc act ttc ccg gat gtg gtg ctt gta cgg gta ccc aca ccc 363

Ala Leu Thr Thr Phe Pro Asp Val Val Leu Val Arg Val Pro Thr Pro

65 70 75

tca gtg cag tca gac agt gac atc act gtc ctg cga cac ctg gag aag 411

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Ser Val Gln Ser Asp Ser Asp Ile Thr Val Leu Arg His Leu Glu Lys

80

85

90

ctg ggc tgc cgg ttg gtc aat cgc cca cag agc atc tta aat tgc atc 459

Leu Gly Cys Arg Leu Val Asn Arg Pro Gln Ser Ile Leu Asn Cys Ile

95

100

105

aac aaa ttc tgg acg ttc caa gaa ctg gct gga cat ggg gtc ccc atg 507

Asn Lys Phe Trp Thr Phe Gln Glu Leu Ala Gly His Gly Val Pro Met

110

115

120

125

cca gac acc ttc tcc tat ggt ggg cat gaa gac ttt tca aaa atg att 555

Pro Asp Thr Phe Ser Tyr Gly Gly His Glu Asp Phe Ser Lys Met Ile

130

135

140

gat gaa gct gag ccc ctg ggc tac cca gtc gtg gtg aag agc aca cga 603

Asp Glu Ala Glu Pro Leu Gly Tyr Pro Val Val Val Lys Ser Thr Arg

145

150

155

ggc cac cgg gga aaa gct gtt ttt ctg gca aga gat aaa cat cac ctc 651

Gly His Arg Gly Lys Ala Val Phe Leu Ala Arg Asp Lys His His Leu

160

165

170

tct gac atc tgc cat ctg atc cgc cac gat gtg ccc tac ctg ttc cag 699

Ser Asp Ile Cys His Leu Ile Arg His Asp Val Pro Tyr Leu Phe Gln

175

180

185

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aag tac gtg aag gag tcc cat gga aag gac atc cgg gtg gtg gtg gta 747
 Lys Tyr Val Lys Glu Ser His Gly Lys Asp Ile Arg Val Val Val Val
 190 195 200 205

ggg ggc cag gtc ata ggc tct atg ctt cgc tgc tcc act gat gga cgg 795
 Gly Gly Gln Val Ile Gly Ser Met Leu Arg Cys Ser Thr Asp Gly Arg
 210 215 220

atg cag agc aac tgc tct ctc ggt ggc gtg ggc gtc aag tgt ccg ctg 843
 Met Gln Ser Asn Cys Ser Leu Gly Gly Val Gly Val Lys Cys Pro Leu
 225 230 235

aca gaa caa ggc aag cag ttg gct att cag gtg tcc aac atc cta ggc 891
 Thr Glu Gln Gly Lys Gln Leu Ala Ile Gln Val Ser Asn Ile Leu Gly
 240 245 250

atg gac ttc tgt ggc att gat ctc ctt atc atg gac gat ggc tcc ttt 939
 Met Asp Phe Cys Gly Ile Asp Leu Leu Ile Met Asp Asp Gly Ser Phe
 255 260 265

gtg gtg tgt gag gca aat gct aat gtt ggc ttc cta gcc ttt gac cag 987
 Val Val Cys Glu Ala Asn Ala Asn Val Gly Phe Leu Ala Phe Asp Gln
 270 275 280 285

gca tgc aac tta gat gtg ggt ggg atc att gca gac tat acc atg tcc 1035

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Ala Cys Asn Leu Asp Val Gly Gly Ile Ile Ala Asp Tyr Thr Met Ser

290

295

300

ttg ctg cca aat agg cag act gga aag atg gct gtc ctc cca gga ctg 1083

Leu Leu Pro Asn Arg Gln Thr Gly Lys Met Ala Val Leu Pro Gly Leu

305

310

315

tcg agt cca agg gag aag aac gag ccg gat ggc tgt gct tca gct cag 1131

Ser Ser Pro Arg Glu Lys Asn Glu Pro Asp Gly Cys Ala Ser Ala Gln

320

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330

gga gtt gca gag agc gtc tat acc atc aac agt ggg tct acc tct agc 1179

Gly Val Ala Glu Ser Val Tyr Thr Ile Asn Ser Gly Ser Thr Ser Ser

335

340

345

gaa agt gag cct gaa ctg gga gag atc cgg gat tcc tca gca agc aca 1227

Glu Ser Glu Pro Glu Leu Gly Glu Ile Arg Asp Ser Ser Ala Ser Thr

350

355

360

365

atg ggg gcc cca ccc tcc atg ctg ccc gaa cct ggc tac aac att aac 1275

Met Gly Ala Pro Pro Ser Met Leu Pro Glu Pro Gly Tyr Asn Ile Asn

370

375

380

aac agg att gct tct gag tta aaa ctt aag tga attcctgctt tttaggcagca 1328

Asn Arg Ile Ala Ser Glu Leu Lys Leu Lys

385

390

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tttaaacc aa atcctactgc ttcctagta gtttigagt aataaaatct ggactaatgt 1388

gatttcattt gcacagaaac tagaaatccc atctgggcac tcagcatttt ttctaacgat 1448

gatttaagca aatggcctag ctttgtggtt ttacaaaga caaatataaa aacactcaca 1508

agaacaaaaa aaaaaaaaaa 1528

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<213> Homo sapiens

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1

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15

Tyr Pro Gln Val Gln Ile Leu Arg Ala Leu Arg Gln Arg Cys Ser Glu

20

25

30

Gln Asp Val Arg Phe Arg Ala Val Leu Met Asp Gln Ile Ala Val Thr

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35

40

45

Ile Val Gly Gly His Leu Gly Leu Gln Leu Asn Gln Lys Ala Leu Thr

50

55

60

Thr Phe Pro Asp Val Val Leu Val Arg Val Pro Thr Pro Ser Val Gln

65

70

75

80

Ser Asp Ser Asp Ile Thr Val Leu Arg His Leu Glu Lys Leu Gly Cys

85

90

95

Arg Leu Val Asn Arg Pro Gln Ser Ile Leu Asn Cys Ile Asn Lys Phe

100

105

110

Trp Thr Phe Gln Glu Leu Ala Gly His Gly Val Pro Met Pro Asp Thr

115

120

125

Phe Ser Tyr Gly Gly His Glu Asp Phe Ser Lys Met Ile Asp Glu Ala

130

135

140

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Glu Pro Leu Gly Tyr Pro Val Val Val Lys Ser Thr Arg Gly His Arg
145 150 155 160

Gly Lys Ala Val Phe Leu Ala Arg Asp Lys His His Leu Ser Asp Ile
165 170 175

Cys His Leu Ile Arg His Asp Val Pro Tyr Leu Phe Gln Lys Tyr Val
180 185 190

Lys Glu Ser His Gly Lys Asp Ile Arg Val Val Val Val Gly Gly Gln
195 200 205

Val Ile Gly Ser Met Leu Arg Cys Ser Thr Asp Gly Arg Met Gln Ser
210 215 220

Asn Cys Ser Leu Gly Gly Val Gly Val Lys Cys Pro Leu Thr Glu Gln
225 230 235 240

Gly Lys Gln Leu Ala Ile Gln Val Ser Asn Ile Leu Gly Met Asp Phe

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245

250

255

Cys Gly Ile Asp Leu Leu Ile Met Asp Asp Gly Ser Phe Val Val Cys

260

265

270

Glu Ala Asn Ala Asn Val Gly Phe Leu Ala Phe Asp Gln Ala Cys Asn

275

280

285

Leu Asp Val Gly Gly Ile Ile Ala Asp Tyr Thr Met Ser Leu Leu Pro

290

295

300

Asn Arg Gln Thr Gly Lys Met Ala Val Leu Pro Gly Leu Ser Ser Pro

305

310

315

320

Arg Glu Lys Asn Glu Pro Asp Gly Cys Ala Ser Ala Gln Gly Val Ala

325

330

335

Glu Ser Val Tyr Thr Ile Asn Ser Gly Ser Thr Ser Ser Glu Ser Glu

340

345

350

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Pro Glu Leu Gly Glu Ile Arg Asp Ser Ser Ala Ser Thr Met Gly Ala
355 360 365

Pro Pro Ser Met Leu Pro Glu Pro Gly Tyr Asn Ile Asn Asn Arg Ile
370 375 380

Ala Ser Glu Leu Lys Leu Lys
385 390

<210> 3

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<212> DNA

<213> Artificial

<220>

<223> An artificially synthesized primer sequence for RT-PCR

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acaacagcct caagatcatc ag

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1 1 / 2 7

<211> 20

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ggtcaccac tgacacgttg

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caaataggca gactggaaag atg

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<211> 23

<212> DNA

1 2 / 2 7

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<400> 6

ctagggaagc agtaggattt ggt

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<211> 30

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<212> DNA

<213> Artificial

1 3 / 2 7

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36

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<211> 22

<212> DNA

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tggtagccaa gtgcaggtta ta

22

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<211> 22

<212> DNA

<213> Artificial

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1 4 / 2 7

<400> 10

ccaaagggtt tctgcagttt ca

22

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<212> DNA

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<400> 11

tgcggatcca gagcagattg tactgagagt

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<210> 12

<211> 29

<212> DNA

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<400> 12

1 5 / 2 7

ctctatctcg agtgaggcgg aaagaacca

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<210> 13

<211> 47

<212> DNA

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<223> An artificially synthesized primer sequence for RT-PCR

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tttaagcttg aagaccattt ttggaaaaaa aaaaaaaaaa aaaaaaac

47

<210> 14

<211> 34

<212> DNA

<213> Artificial

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<223> An artificially synthesized primer sequence for RT-PCR

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34

1 6 / 2 7

<210> 15

<211> 51

<212> DNA

<213> Artificial

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caccgaagca gcacgacttc ttcttcaaga gagaagaagt cgtgctgctt c 51

<210> 16

<211> 51

<212> DNA

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<400> 16

aaaagaagca gcacgacttc ttctctcttg aagaagaagt cgtgctgctt c 51

<210> 17

1 7 / 2 7

<211> 51

<212> DNA

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<210> 18

<211> 51

<212> DNA

<213> Artificial

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<223> An artificially synthesized oligonucleotide sequence for siRNA

<400> 18

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<210> 19

<211> 19

<212> DNA

18 / 27

<213> Artificial

<220>

<223> An artificially synthesized target sequence for siRNA

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gtgtccgctg acagaacaa

19

<210> 20

<211> 21

<212> DNA

<213> Artificial

<220>

<223> An artificially synthesized primer sequence for RT-PCR

<400> 20

gagctcctga accatctgct c

21

<210> 21

<211> 23

<212> DNA

<213> Artificial

1 9 / 2 7

<220>

<223> An artificially synthesized primer sequence for RT-PCR

<400> 21

caagatgtac agagcatcac agc

23

<210> 22

<211> 29

<212> DNA

<213> Artificial

<220>

<223> An artificially synthesized primer sequence for RT-PCR

<400> 22

attgaattcg catggcgcca cccgcggcg

29

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<212> DNA

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<223> An artificially synthesized primer sequence for RT-PCR

20 / 27

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aatggtacct caccaaggcc tccagacact cc

32

<210> 24

<211> 51

<212> DNA

<213> Artificial

<220>

<223> An artificially synthesized oligonucleotide sequence for siRNA

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<210> 25

<211> 51

<212> DNA

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<220>

<223> An artificially synthesized oligonucleotide sequence for siRNA

<400> 25

2 1 / 2 7

aaaaactttt agggaccctg cagtctcttg aactgcaggg tccctaaaag t

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<210> 26

<211> 19

<212> DNA

<213> Artificial

<220>

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acttttaggg accctgcag

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<210> 27

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<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (125).. (799)

<223>

<400> 27

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ccgggtccccg ccgCtccccg tccccgctgc tcctagcccc tgccgcgtcc ccggcggagc 120

gggc atg gcg cca ccc gcg gcg cct ggc cgg gac cgt gtg ggc cgt gag 169

Met Ala Pro Pro Ala Ala Pro Gly Arg Asp Arg Val Gly Arg Glu

1

5

10

15

gat gag gac ggc tgg gag acg cga ggg gac cgc aag gcc cgg aag ccc 217

Asp Glu Asp Gly Trp Glu Thr Arg Gly Asp Arg Lys Ala Arg Lys Pro

20

25

30

ctg gtg gag aag aag cgg cgc gcg cgg atc aac gag agc ctg cag gag 265

Leu Val Glu Lys Lys Arg Arg Ala Arg Ile Asn Glu Ser Leu Gln Glu

35

40

45

ctg cgg ctg ctg ctg gcg ggc gcc gag gtg cag gcc aag ctg gag aac 313

Leu Arg Leu Leu Leu Ala Gly Ala Glu Val Gln Ala Lys Leu Glu Asn

50

55

60

gcc gaa gtg ctg gag ctg acg gtg cgg cgg gtc cag ggt gtg ctg cgg 361

Ala Glu Val Leu Glu Leu Thr Val Arg Arg Val Gln Gly Val Leu Arg

65

70

75

ggc cgg gcg cgc gag cgc gag cag ctg cag gcg gaa gcg agc gag cgc 409

Gly Arg Ala Arg Glu Arg Glu Gln Leu Gln Ala Glu Ala Ser Glu Arg

2 3 / 2 7

80

85

90

95

ttc gct gcc ggc tac atc cag tgc atg cac gag gtg cac acg ttc gtg 457

Phe Ala Ala Gly Tyr Ile Gln Cys Met His Glu Val His Thr Phe Val

100

105

110

tcc acg tgc cag gcc atc gac gct acc gtc gct gcc gag ctc ctg aac 505

Ser Thr Cys Gln Ala Ile Asp Ala Thr Val Ala Ala Glu Leu Leu Asn

115

120

125

cat ctg ctc gag tcc atg ccg ctg cgt gag ggc agc agc ttc cag gat 553

His Leu Leu Glu Ser Met Pro Leu Arg Glu Gly Ser Ser Phe Gln Asp

130

135

140

ctg ctg ggg gac gcc ctg gcg ggg cca cct aga gcc cct gga cgg agt 601

Leu Leu Gly Asp Ala Leu Ala Gly Pro Pro Arg Ala Pro Gly Arg Ser

145

150

155

ggc tgg cct gcg ggg ggc gct ccg gga tcc cca ata ccc agc ccc ccg 649

Gly Trp Pro Ala Gly Gly Ala Pro Gly Ser Pro Ile Pro Ser Pro Pro

160

165

170

175

ggt cct ggg gac gac ctg tgc tcc gac ctg gag gag gcc cct gag gct 697

Gly Pro Gly Asp Asp Leu Cys Ser Asp Leu Glu Glu Ala Pro Glu Ala

180

185

190

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gaa ctg agt cag gct cct gct gag ggg ccc gac ttg gtg ccc gca gcc 745

Glu Leu Ser Gln Ala Pro Ala Glu Gly Pro Asp Leu Val Pro Ala Ala

195

200

205

ctg ggc agc ctg acc aca gcc caa att gcc cgg agt gtc tgg agg cct 793

Leu Gly Ser Leu Thr Thr Ala Gln Ile Ala Arg Ser Val Trp Arg Pro

210

215

220

tgg tga ccaatgccag ccagagtcct gcgggggtgg gcccggccct ccctggatct 849

Trp

cctccctcct cccagggggt cagatgttgt ggggtagggc cctggaagtc tcccaggctt 909

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cccagccccg tttcttaaga aacttttagg gaccctgcag ctctggagtg ggtggaggga 1029

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accagccctt caccagccct gtgcgggctc tgggggcaga ggtggcagga atggtgcttg 1149

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2 5 / 2 7

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taaagaattt tggagttagt tacccttgaa aaaaaaaaaa aaaaaa 1375

<210> 28

<211> 224

<212> PRT

<213> Homo sapiens

<400> 28

Met Ala Pro Pro Ala Ala Pro Gly Arg Asp Arg Val Gly Arg Glu Asp

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Glu Asp Gly Trp Glu Thr Arg Gly Asp Arg Lys Ala Arg Lys Pro Leu

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Val Glu Lys Lys Arg Arg Ala Arg Ile Asn Glu Ser Leu Gln Glu Leu

35 40 45

Arg Leu Leu Leu Ala Gly Ala Glu Val Gln Ala Lys Leu Glu Asn Ala

50 55 60

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Glu Val Leu Glu Leu Thr Val Arg Arg Val Gln Gly Val Leu Arg Gly
65 70 75 80

Arg Ala Arg Glu Arg Glu Gln Leu Gln Ala Glu Ala Ser Glu Arg Phe
 85 90 95

Ala Ala Gly Tyr Ile Gln Cys Met His Glu Val His Thr Phe Val Ser
 100 105 110

Thr Cys Gln Ala Ile Asp Ala Thr Val Ala Ala Glu Leu Leu Asn His
 115 120 125

Leu Leu Glu Ser Met Pro Leu Arg Glu Gly Ser Ser Phe Gln Asp Leu
 130 135 140

Leu Gly Asp Ala Leu Ala Gly Pro Pro Arg Ala Pro Gly Arg Ser Gly
145 150 155 160

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Trp Pro Ala Gly Gly Ala Pro Gly Ser Pro Ile Pro Ser Pro Pro Gly

165

170

175

Pro Gly Asp Asp Leu Cys Ser Asp Leu Glu Glu Ala Pro Glu Ala Glu

180

185

190

Leu Ser Gln Ala Pro Ala Glu Gly Pro Asp Leu Val Pro Ala Ala Leu

195

200

205

Gly Ser Leu Thr Thr Ala Gln Ile Ala Arg Ser Val Trp Arg Pro Trp

210

215

220